

12/18

Fig. 11-2

401 CTCCCTACTGGAACGCACCTCTGTGAGGTTGAAACAGATAAGGAATGGACCT 450
 401 CTCCCTACTGGAACGCACCTCTGTGAGGTTGAAACAGATAAGGAATGGACCT 450
 451 CCAGTCATTCAATTCTGGAATCAAAGACCTAAAAGTCTTGAACACCAACCCCA 500
 451 CCAGTCATTCAATTCTGGAATCAAAGACCTAAAAGTCTTGAACACCAACCCCA 500
 501 GTCTGGCTTGAAGGATTCAAGGACCAAGTCACCACCCCTCCCTGAGG 550
 501 GTCTGGCTTGAAGGATTCAAGGACCAAGTCACCACCCCTCCCTGAGG 550
 551 TGAAGGACCGGTGCTTGCCACCCAAAGTGTACTGCAAATGGCGCTACCCAC 600
 551 TGAAGGACCGGTGCTTGCCACCCAAAGTGTACTGCAAATGGCGCTACCCAC 600
 601 CAGGGCAGAGATGTGGACTTGAGGCCACCTGGGACACTGTAGGAGCAT 650
 601 CAGGGCAGAGATGTGGACTTGAGGCCACCTGGGACACTGTAGGAGCAT 650
 651 TGTCCTGCAGAAATTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
 651 TGTCCTGCAGAAATTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
 701 CTGTCAGAAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
 701 CTGTCAGAAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
 751 CCTGAGATAGAAGATATGGAATCAGCCTGCCAAATATTCACTACTTAAA 800
 751 CCTGAGATAGAAGATATGGAATCAGCCTGCCAAATATTCACTACTTAAA 800
 801 CATAGACATGCCAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
 801 CATAGACATGCCAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
 851 CTTTAGACAACTCCATATGGAAAAATTACTGGTACAGTCAGAGGAAGTTG 900
 851 CTTTAGACAACTCCATATGGCAGGATTACTGGTACAGTCAGAGGAAGCTG 900
 901 TCTTCAAGACTGTGA 915
 901 ACTTCAAGGCTGTGA 915

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Fig. 12-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of Pig KS uricase ("PKS") vs. baboon uricase

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Gap Weight: 50 Average Match: 10.000
 Length Weight: 3 Average Mismatch: -9.000

Quality: 7573 Length: 915
 Ratio: 8.277 Gaps: 0
 Percent Similarity: 90.929 Percent Identity: 90.929

Match display thresholds for the alignment(s):
 | = IDENTITY
 : = 5
 . = 1

pigKS.seq x baboon.seq July 25, 1998 10:21 ..

PKS	1	ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTGT	50
bab	1	ATGGCCGACTACCATAACAACTATAAAAAGAATGATGAATTGGAGTTGT	50
	51	CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCA CGCAG	100
	51	CCGAACTGGCTATGGGAAGGATATGGTAAAAGTTCTCCATATTCA CGCAG	100
	101	ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGC AACTGACT	150
	101	ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGC AACTTACT	150
	151	TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCA GAGATGTCATCC	200
	151	CTGAGTTCCAAAAAGATTACCTGCATGGAGATAATTCA GAGATATCATCC	200
	201	TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA	250
	201	TACAGACACCATCAAGAACACAGTTAATGTCCTGGCAAAGTTAAGGGAA	250
	251	TCAAAAGCATAGAACATTGGCTGTGACTATCTGTGAGCATTCTTTCT	300
	251	TCAAAAGCATAGAACGGCTTGGTGTGAATATTGTGAGTATTCTTTCT	300
	301	TCCTTCAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGGAAGTTCTTG	350
	301	TCTTTAACCATGTAATCCGAGCTCAAGTCTACGTGGAAGAAATCCCTG	350
	351	GAAGCGTTGAAAAGAATGGAGTTAACGATGTCCATGCATTATTTATA	400
	351	GAAGCGTCTGAAAAGAATGGAGTTAACGATGTCCATGCATTATTCACA	400

Fig. 12-2

401 CTCCTACTGGAACGCACTCTGTGAGGTTGAAACAGATAAGGAATGGACCT 450
 401 ||||| ||||| |||||
 401 CTCCCCTGAAACACACTCTGTGAAAGTGAACAACGTGAGAAGTGGACCC 450
 451 CCAGTCATTCAATTCTGGAATCAAAGACCTAAAAGTCTTGAAGAACACCA 500
 451 ||||| |||||
 451 CCCGTCAATTCAATTCTGGAATCAAAGACCTCAAGGTCTTGAAGAACACA 500
 501 GTCTGGTTTGAAGGATTCAAGGACCAAGTTCACCCCTCCCTGAGG 550
 501 ||||| |||||
 501 GTCTGGATTGAAGGTTTCAAGGACCAAGTTCACCCCTCCCTGAGG 550
 551 TGAAGGACCGGTGCTTGGCACCCAAAGTGTACTGCAATGGCGCTACAC 600
 551 ||||| |||||
 551 TGAAGGACCGATGCTTGGCACCCAAAGTGTACTGCAATGGCGCTACAC 600
 601 CAGGGCAGAGATGTGGACTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
 601 ||||| |||||
 601 CAGTGCAGGGATGTGGACTTCAGGCTACCTGGGGCACCATCGGGACCT 650
 651 TGTCTGCAGAAATTGCTGGCCCTATGACAAGGGAGTACTCGCCCT 700
 651 ||||| |||||
 651 TGTCTGGAGAAATTGCTGGCCCTATGACAAGGGAGTACTCACCCCT 700
 701 CTGTCCAGAAGACACTCTATGACATCCAGGTGCTCACCCCTGGGCAGTT 750
 701 ||||| |||||
 701 CTGTGCAGAAGACCCCTATGATATCCAGGTGCTCTCCCTGAGCCGAGTT 750
 751 CCTGAGATAGAAGATATGAAATCAGCCTGCCAAATATTCACTACTTAA 800
 751 ||||| |||||
 751 CCTGAGATAGAAGATATGAAATCAGCCTGCCAAACATTCACACTACTCAA 800
 801 CATAGACATGCCAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
 801 ||||| |||||
 801 TATAGACATGCCAAATGGGTCTGATCAACAAGGAAGAGGTCTTGCTGC 850
 851 CTTTAGACAATCCATATGAAAAAATTACTGGTACACTCAAGAGGAAGTTG 900
 851 ||||| |||||
 851 CATTAGACAATCCATATGAAAAAATTACTGGTACACTCAAGAGGAAGTTG 900
 901 TCTTCAAGACTGTGA 915
 901 ||||| |||||
 901 TCTTCAAGACTGTGA 915